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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/691,731	10/23/2003	Cornelia Berghof	930008-2023.1	8400
20999 7590 02/22/2007 FROMMER LAWRENCE & HAUG 745 FIFTH AVENUE- 10TH FL. NEW YORK, NY 10151			EXAMINER SITTON, JEHANNE SOUAYA	
			ART UNIT 1634	PAPER NUMBER
SHORTENED STATUTORY PERIOD OF RESPONSE			MAIL DATE	DELIVERY MODE
3 MONTHS			02/22/2007	PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

**Office Action Summary**

Application No.

10/691,731

Applicant(s)

BERGHOF ET AL.

Examiner

Jehanne S. Sitton

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 22 November 2006.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 21-28 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 21-28 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)          | 4) <input type="checkbox"/> Interview Summary (PTO-413)           |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____                                      |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)          | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date _____  | 6) <input type="checkbox"/> Other: _____                          |

## **DETAILED ACTION**

### ***Election/Restrictions***

1. The previous election of species requirement required election to a specific combination of SEQ ID NOS. Although the response filed 11/22/2006 did not properly reply to the election of species requirement in that no specific species, that is specific combination of sequences, was elected, the election of species requirement is hereby withdrawn in view of applicant's arguments that the "claims, as originally filed, and presented herein, represent obvious variants of the same sequence, namely SEQ ID NO: 1 of WO 95/00664" (page 5, para 4) of the response. In view of such argument, the following rejections are set forth below.

### ***Specification***

The following guidelines illustrate the preferred layout for the specification of a utility application. These guidelines are suggested for the applicant's use.

### **Arrangement of the Specification**

As provided in 37 CFR 1.77(b), the specification of a utility application should include the following sections in order. Each of the lettered items should appear in upper case, without underlining or bold type, as a section heading. If no text follows the section heading, the phrase "Not Applicable" should follow the section heading:

- (a) TITLE OF THE INVENTION.
- (b) CROSS-REFERENCE TO RELATED APPLICATIONS.
- (c) STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT.
- (d) THE NAMES OF THE PARTIES TO A JOINT RESEARCH AGREEMENT.
- (e) INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ON A COMPACT DISC.
- (f) BACKGROUND OF THE INVENTION.
  - (1) Field of the Invention.
  - (2) Description of Related Art including information disclosed under 37 CFR 1.97 and 1.98.
- (g) BRIEF SUMMARY OF THE INVENTION.
- (h) BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWING(S).
- (i) DETAILED DESCRIPTION OF THE INVENTION.

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- (j) CLAIM OR CLAIMS (commencing on a separate sheet).
- (k) ABSTRACT OF THE DISCLOSURE (commencing on a separate sheet).
- (l) SEQUENCE LISTING (See MPEP § 2424 and 37 CFR 1.821-1.825. A "Sequence Listing" is required on paper if the application discloses a nucleotide or amino acid sequence as defined in 37 CFR 1.821(a) and if the required "Sequence Listing" is not submitted as an electronic document on compact disc).

***Claim Rejections - 35 USC § 112***

2. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

3. Claims 21-28 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to nucleic acids molecules which need be identical to the recited SEQ ID NOS: in 10 contiguous or 15 contiguous nucleotides, as well as to nucleic acid molecules that comprise the indicated SEQ ID NOS or their complements which are to be used in nucleic acid hybridization or amplification to detect all representatives of *Salmonella enterica* subspecies: *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenai*, *bongori*, and *indica*. The claims encompass a large genus of nucleic acid molecules including allelic variants and mutants of the recited SEQ ID NOS as well as genomic sequences which comprise the indicated SEQ ID NOS. The specification discloses the sequences of SEQ ID NOS 1-10 and teaches that the sequences are identical or altered with respect to a specific region of a fragment of *Salmonella typhimurium*.

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LT2 chromosome which is taught by Holmes et al in WO9500664 (the fragment is denoted as SEQ ID NO 1 in WO9500664). Holmes et al, however, do not teach the complete sequence of the LT2 chromosome or whether SEQ ID NO 1 is a sequence within a specific gene, or intervening sequence. Therefore, the recitation of "comprising" (which is considered 'open' language) and the minimal length of "10 contiguous nucleotides", and "15 contiguous" encompasses partial genomic sequences of undetermined length (not defined by the specification) as well as complete genes from any serotype of *Salmonella* which have not been taught or described by the specification. The disclosed structural features of SEQ ID NOS 1-10, however, do not represent a substantial portion of the claimed genomic sequences, genes, variants, or homologues. The claimed limitation that the sequences are used to detect all representatives of *Salmonella enterica* subspecies *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae*, *bongori*, and *indica* is not adequate to describe other relevant identifying characteristics of the claimed genus because the specification has not described any distinguishing characteristics of the undisclosed possible additional sequences which are encompassed by the claims that would allow the detection of all representatives of *Salmonella enterica* subspecies *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae*, *bongori*, and *indica*. It is noted that the claims also encompass the complete *S. Typhimurium* LT2 chromosome, but that such was not taught in either the specification or the art at the time the invention was filed. The sequence of the LT2 chromosome was first disclosed by McClelland et al (Nature, vol. 413, 2001, pp 852-856). Further, McClelland teaches that *S. Bongori* and *S. Arizonae* share 85% and 83% homology with coding sequences of the LT2 chromosome, illustrating that considerable variability exists between the different species. However the specification has not taught or

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described the identity of sequences which could additionally be used to detect the different *Salmonella* species recited in the claims, nor has the specification provided an alignment of the chromosomes of the different *Salmonella* species recited such that the skilled artisan would be able to determine which sequences could be used to detect all representatives of *Salmonella enterica* subspecies recited.

Isolated nucleic acids consisting of a sequence from the group consisting of SEQ ID NOS 1-9 and 10 and complements of such meet the written description provisions of 35 USC 112, first paragraph. However, the claims are directed to and encompass full length genes, genomic sequences, variants and homologs, none of which meet the written description provision of 35 USC 112, first paragraph. The specification provides insufficient written description to support the genus encompassed by the claim.

#### ***Claim Rejections - 35 USC § 102***

4. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

5. Claim 22 is rejected under 35 U.S.C. 102(b) as being anticipated by Brennan (US Patent 5,474,796).

The claimed recitation of “consisting essentially of” has been interpreted as “comprising” because the specification does not clearly point out what is essential to the claimed set of nucleic acid molecules. Accordingly, the set is broadly interpreted to encompass more than 2 nucleic

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acid molecules. Brennan teaches constructing an array of every possible 10 mer nucleic acid sequence (cols 9 and 10), which anticipates the broadly claimed recitation of a set of nucleic acid molecules which encompasses 10 mer nucleotide sequences.

6. Claims 22-28 are rejected under 35 U.S.C. 102(b) as being anticipated by Holmes (Holmes et al; WO 95/00664).

The claimed recitation of “consisting essentially of” has been interpreted as “comprising” because the specification does not clearly point out what is essential to the claimed set of nucleic acid molecules. Accordingly, the set is broadly interpreted to encompass more than 2 nucleic acid molecules. Holmes teaches obtaining a nucleic acid molecule, SEQ ID NO: 1, which comprises a number of the instantly recited SEQ ID NOS (SEQ ID NO: 1, 3, 6, and 9). Accordingly, more than one copy of SEQ ID NO: 1, which is inherently taught by Holmes (page 2, last full para) inherently anticipates a set of nucleic acid molecules which comprise at least 2 of the recited SEQ ID NOS. With regard to claims 23-25, the molecules taught by Holmes inherently comprise at least 15 or 20 contiguous nucleotides of the recited SEQ ID NOS, as well as containing additional sequence. With regard to claim 26, the term ‘contains’ is broadly interpreted as comprising. The molecules taught by Holmes inherently comprise 15-30 nucleotides. With regard to claims 27-28, the sequence contains a free 3’ end for extension with a polymerase and is interpreted to contain a group allowing for a direct enzyme reaction.

***Claim Rejections - 35 USC § 103***

7. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

8. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

9. Claims 21-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Holmes (Holmes et al; WO 95/00664).

The claims are drawn to a set of isolated nucleic acid molecules wherein each nucleic acid molecule comprises at least 10, 15, or 20 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS 1-10 and the complementary sequence of SEQ ID NO: 1-10, wherein the set consists essentially of two sequences. It is noted that the recitation of "the set consists essentially of" has been interpreted to encompass "comprising" because the specification does not particular point out which features are considered 'essential' to the set of nucleic acids. Although the set is recited to be used in nucleic acid hybridization or amplification to detect all representatives of *Salmonella enterica* subspecies: *enterica*, *salamae*,

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*arizonae*, *diarizonae*, *houtenai*, *bongori*, and *indica*, the use for the set has been given no patentable weight. The following rejection is set forth based on the interpretation that the claimed set is to 2 or more different nucleic acid molecules.

Holmes teaches an invention which provides nucleic acid molecules for the detection and identification of *Salmonella* species, and for detecting one or more *Salmonella* serotypes and to kits comprising these nucleic acid molecules (see abstract). Holmes teaches a need for detecting *Salmonella* because the incidence of salmonellosis has increased significantly during the last two decades in western countries and that while standard culture methods are still widely used for detection of *Salmonella* in foods, the control of infection depends on the availability of rapid and precise tests for monitoring of primary animal production (see p. 1). Holmes teaches that nucleic acid based methods for detection of a DNA or RNA from a target organism have proliferated and that the invention of Holmes is based on using certain fragments of the *Salmonella* typhimurium LT2 chromosome (or corresponding nucleic acid fragments having the same sequence of bases, including RNA, PNA, etc) as primers in PCR and other amplification systems, in particular certain fragments corresponding to regions of the genome which are highly conserved in *Salmonella* species (see paragraph bridging pages 2 and 3). Holmes teaches the sequence of SEQ ID NO: 1, which is a fragment of the LT2 chromosome. With regard to claims 23-26, Holmes teaches constructing nucleic acid molecules as primers and probes (page 5, last para, and sequences bridging pages 4-5) which have 15-30 as well as preferably 20 bases, for *Salmonella* detection. Holmes teaches specifically teaches using PCR and sets of 2 or more nucleotide molecules for detection (see p. 14, 15, and table 1,2 and 3, examples 1 and 2). With regard to

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claims 27-28, the primers contains a free 3' end for extension with a polymerase and are interpreted to contain a group allowing for a direct enzyme reaction (page 6, last full para).

Although Holmes does not teach a set of at least two different nucleic acid molecules , which comprise 10, 15, or 20 contiguous nucleotides of the recited SEQ ID NOS, Holmes provide motivation for the ordinary artisan to construct sets of nucleic acid molecules for use as primers and probes for Salmonella detection, as set forth above, and arrive at sets of nucleic acid molecules encompassed by the claimed invention. Therefore it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to construct sequences as Holmes teaches how to construct nucleic acid molecules for the purpose of detecting Salmonella, and teaches the use of SEQ ID NO 1 of Holmes to construct such sequences. As noted by applicant's in the response dated the "claims, as originally filed, and presented herein, represent obvious variants of the same sequence, namely SEQ ID NO: 1 of WO 95/00664" (page 5, para 4) of the response.

10. Claims 21-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Holmes in view of Hogan et al. (US Pat. 5,541,308, July 30, 1996).

The claims are drawn to a set of isolated nucleic acid molecules wherein each nucleic acid molecule comprises at least 10, 15, or 20 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOS 1-10 and the complementary sequence of SEQ ID NO: 1-10, wherein the set consists essentially of two sequences. It is noted that the recitation of "the set consists essentially of" has been interpreted to encompass "comprising" because the specification does not particular point out which features are considered 'essential' to the set of

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nucleic acids. Although the set is recited to be used in nucleic acid hybridization or amplification to detect all representatives of *Salmonella enterica* subspecies: *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenai*, *bongori*, and *indica*, the use for the set has been given no patentable weight. The following rejection is set forth based on the interpretation that the claimed set is to 2 or more different nucleic acid molecules.

Holmes teaches an invention which provides nucleic acid molecules for the detection and identification of *Salmonella* species, and for detecting one or more *Salmonella* serotypes and to kits comprising these nucleic acid molecules (see abstract). Holmes teaches a need for detecting *Salmonella* because the incidence of salmonellosis has increased significantly during the last two decades in western countries and that while standard culture methods are still widely used for detection of *Salmonella* in foods, the control of infection depends on the availability of rapid and precise tests for monitoring of primary animal production (see p. 1). Holmes teaches that nucleic acid based methods for detection of a DNA or RNA from a target organism have proliferated and that the invention of Holmes is based on using certain fragments of the *Salmonella typhimurium* LT2 chromosome (or corresponding nucleic acid fragments having the same sequence of bases, including RNA, PNA, etc) as primers in PCR and other amplification systems, in particular certain fragments corresponding to regions of the genome which are highly conserved in *Salmonella* species (see paragraph bridging pages 2 and 3). Holmes teaches the sequence of SEQ ID NO: 1, which is a fragment of the LT2 chromosome. With regard to claims 23-26, Holmes teaches constructing nucleic acid molecules as primers and probes (page 5, last para, and sequences bridging pages 4-5) which have 15-30 as well as preferably 20 bases, for *Salmonella* detection. Holmes teaches specifically teaches using PCR and sets of 2 or more nucleotide

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molecules for detection (see p. 14, 15, and table 1,2 and 3, examples 1 and 2). With regard to claims 27-28, the primers contains a free 3' end for extension with a polymerase and are interpreted to contain a group allowing for a direct enzyme reaction (page 6, last full para).

Although Holmes does not teach a set of at least two different nucleic acid molecules , which comprise 10, 15, or 20 contiguous nucleotides of the recited SEQ ID NOS, Holmes provide motivation for the ordinary artisan to construct sets of nucleic acid molecules for use as primers and probes for Salmonella detection, as set forth above, and arrive at sets of nucleic acid molecules encompassed by the claimed invention. Further, Hogan teaches the use of specific primers col. 6-7, lines 50-67, lines 1-12, and furthermore provides specific guidance for the selection of hybridizing oligonucleotides:

"Once the variable regions are identified, the sequences are aligned to reveal areas of maximum homology or 'match'. At this point, the sequences are examined to identify potential probe regions. Two important objectives in designing a probe are to maximize homology to the target sequence(s) (greater than 90% homology is recommended) and to minimize homology to non-target sequence(s) (less than 90% homology to non-targets is recommended). We have identified the following useful guidelines for designing probes with the desired characteristics. First, probes should be positioned so as to minimize the stability of the probe:nontarget nucleic acid hybrid. This may be accomplished by minimizing the length of perfect complementarity to non-target organisms, avoiding G and C rich regions of homology to non-target sequences, and by positioning the probe to span as many destabilizing mismatches as possible (for example, dG:rU base pairs are less destabilizing than some others). Second, the stability of the probe:target nucleic acid hybrid should be maximized. This may be accomplished by avoiding long A and T rich sequences, by terminating the hybrids with G:C base pairs and by designing the probe with an appropriate T<sub>m</sub>. The beginning and end points of the probe should be chosen so that the length and %G and %C result in a T<sub>m</sub> about 2-10°C higher than the temperature at which the final assay will be performed. The importance and effect of various assay conditions will be explained further herein. Third, regions of the rRNA which are known to form strong structures inhibitory to hybridization are less preferred. Finally, probes with extensive self complementarity should be avoided."

Hogan teaches that "while oligonucleotide probes of different lengths and base composition may be used, oligonucleotide probes preferred in this invention are between about

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15 and about 50 bases in length" (col. 10, lines 13-15). Hogan teaches that oligonucleotide probes may be labeled by any of several well known methods such as radioisotopes, non-radioactive reporting groups, non-isotopic materials such as fluorescent molecules (col. 10, lines 45-60). Hogan teaches that probes may be labeled using a variety of labels, as described within, and may be incorporated into diagnostic kits.

Therefore it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to construct sequences for the detection of Salmonella as taught by Holmes, including sequences which meet the limitations of the instantly recited claims, in view of the teachings in the prior art and the high level of skill in the art with regard to designing primers and probes for nucleic acid detection methods as exemplified by the teachings of Holmes and Hogan. Holmes teaches how to construct nucleic acid molecules for the purpose of detecting Salmonella, and teaches the use of SEQ ID NO 1 of Holmes to construct such sequences. Designing primers and probes which are equivalents to those taught in the art is routine experimentation. The prior art teaches the parameters and objectives involved in the selection of oligonucleotides that function as probes and primers, see Hogan. Moreover there are many internet web sites that provide free downloadable software to aid in the selection of primers drawn from genetic data recorded in a spreadsheet. The prior art is replete with guidance and information necessary to permit the ordinary artisan in the field of nucleic acid detection to design primers and probes.

### ***Double Patenting***

11. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or

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improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

12. Claims 21-28 are rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-9 of U.S. Patent No. 6,706,472. Although the conflicting claims are not identical, they are not patentably distinct from each other because they are coextensive in scope. The instantly recited claims are drawn to sets of nucleic acid molecules, comprising 2 nucleic acid molecules which are directed to the sequences of SEQ ID NOS 1-10 and the complements of SEQ ID NO: 1-10. The claims of '472 are directed to methods and kits for using one or more of SEQ ID NOS 1-10 and the complements of SEQ ID NOS 1-10 (SEQ ID NOS are identical). Accordingly, the claims are coextensive in scope and not patentably distinct from each other.

### ***Conclusion***

13. No claims are allowed.

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14. Any inquiry concerning this communication or earlier communications from the examiner should be directed to examiner Jehanne Sitton whose telephone number is (571) 272-0752. The examiner can normally be reached Monday-Thursday from 8:00 AM to 5:00 PM and on alternate Fridays.


If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla, can be reached on (571) 272-0735. The fax phone number for this Group is (571) 273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

  
Jehanne Sitton  
Primary Examiner  
Art Unit 1634

 2/16/07